

SEQUENCE LISTING

<110> Zhou, Qun-Yong
Ehlert, Frederick

<120> Prokineticin Polypeptides, Related
Compositions and Methods

<130> P-UC 5016

<150> 60/245,882

<151> 2000-11-03

<160> 19

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<210> 1

<211> 1377

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (55)...(369)

<400> 1

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Arg Gly Ala Thr Arg Val Ser Ile Met Leu Leu Leu Val Thr Val Ser
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gac tgt gct gtg atc aca ggg gcc tgt gag cgg gat gtc cag tgt ggg      153
Asp Cys Ala Val Ile Thr Gly Ala Cys Glu Arg Asp Val Gln Cys Gly
      20              25              30

gca ggc acc tgc tgt gcc atc agc ctg tgg ctt cga ggg ctg cgg atg      201
Ala Gly Thr Cys Cys Ala Ile Ser Leu Trp Leu Arg Gly Leu Arg Met
      35              40              45

tgc acc ccg ctg ggg cgg gaa ggc gag gag tgc cac ccc ggc agc cac      249
Cys Thr Pro Leu Gly Arg Glu Gly Glu Glu Cys His Pro Gly Ser His
      50              55              60              65

aag gtc ccc ttc ttc agg aaa cgc aag cac cac acc tgt cct tgc ttg      297
Lys Val Pro Phe Phe Arg Lys Arg Lys His His Thr Cys Pro Cys Leu
      70              75              80

ccc aac ctg ctg tgc tcc agg ttc ccg gac ggc agg tac cgc tgc tcc      345

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10016431.10101

Pro Asn Leu Leu Cys Ser Arg Phe Pro Asp Gly Arg Tyr Arg Cys Ser
85 90 95

atg gac ttg aag aac atc aat ttt taggcgcttg cctgggtctca ggataccac 399
Met Asp Leu Lys Asn Ile Asn Phe
100 105

catccttttc tgagcacagc ctggattttt atttctgcca tgaaaccacag ctcccatgac 459
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<210> 2
<211> 105
<212> PRT
<213> Homo sapiens

<400> 2
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Gly Ala Gly Thr Cys Cys Ala Ile Ser Leu Trp Leu Arg Gly Leu Arg
35 40 45
Met Cys Thr Pro Leu Gly Arg Glu Gly Glu Glu Cys His Pro Gly Ser
50 55 60
His Lys Val Pro Phe Phe Arg Lys Arg Lys His His Thr Cys Pro Cys
65 70 75 80
Leu Pro Asn Leu Leu Cys Ser Arg Phe Pro Asp Gly Arg Tyr Arg Cys
85 90 95
Ser Met Asp Leu Lys Asn Ile Asn Phe
100 105

<210> 3
<211> 86
<212> PRT
<213> Homo sapiens

<400> 3

10016431.10101

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			20					25					30		
Pro	Leu	Gly	Arg	Glu	Gly	Glu	Glu	Cys	His	Pro	Gly	Ser	His	Lys	Val
		35				40						45			
Pro	Phe	Phe	Arg	Lys	Arg	Lys	His	His	Thr	Cys	Pro	Cys	Leu	Pro	Asn
	50					55					60				
Leu	Leu	Cys	Ser	Arg	Phe	Pro	Asp	Gly	Arg	Tyr	Arg	Cys	Ser	Met	Asp
65					70					75					80
Leu	Lys	Asn	Ile	Asn	Phe										
				85											

<210> 4
 <211> 1406
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (10)...(333)

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 Leu Pro Pro Leu Leu Leu Thr Pro Arg Ala Gly Asp Ala Ala Val Ile
 15 20 25 30

acc ggg gct tgt gac aag gac tcc caa tgt ggt gga ggc atg tgc tgt 147
 Thr Gly Ala Cys Asp Lys Asp Ser Gln Cys Gly Gly Gly Met Cys Cys
 35 40 45

gct gtc agt atc tgg gtc aag agc ata agg att tgc aca cct atg ggc 195
 Ala Val Ser Ile Trp Val Lys Ser Ile Arg Ile Cys Thr Pro Met Gly
 50 55 60

aaa ctg gga gac agc tgc cat cca ctg act cgt aaa gtt cca ttt ttt 243
 Lys Leu Gly Asp Ser Cys His Pro Leu Thr Arg Lys Val Pro Phe Phe
 65 70 75

ggg cgg agg atg cat cac act tgc cca tgt ctg cca ggc ttg gcc tgt 291
 Gly Arg Arg Met His His Thr Cys Pro Cys Leu Pro Gly Leu Ala Cys
 80 85 90

tta cgg act tca ttt aac cga ttt att tgt tta gcc caa aag 333
 Leu Arg Thr Ser Phe Asn Arg Phe Ile Cys Leu Ala Gln Lys
 95 100 105

taatcgctct ggagtagaaa ccaaagtga atagccacat cttacctgta aagtcttact 393

10016481.1001

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tgtgattgtg ccaaacaaaa aatgtgccag aaagaaatgc tcttgcttcc tcaactttcc 453
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atcttacttt tggatagaaa tatgaagtgt aaggcattat ggaactgggt cttattttccc 573
tgtttgtgtt ttggtttgat ttggcttttt tcttaa atgt caaaaacgta cccatttttca 633
caaaaatgag gaaaataaga atttgatatt ttgttagaaa aacttttttt tttttttctc 693
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<212> PRT
<213> Homo sapiens

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20 25 30
Ala Cys Asp Lys Asp Ser Gln Cys Gly Gly Gly Met Cys Cys Ala Val
35 40 45
Ser Ile Trp Val Lys Ser Ile Arg Ile Cys Thr Pro Met Gly Lys Leu
50 55 60
Gly Asp Ser Cys His Pro Leu Thr Arg Lys Val Pro Phe Phe Gly Arg
65 70 75 80
Arg Met His His Thr Cys Pro Cys Leu Pro Gly Leu Ala Cys Leu Arg
85 90 95
Thr Ser Phe Asn Arg Phe Ile Cys Leu Ala Gln Lys
100 105
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<210> 6
<211> 81
<212> PRT
<213> Homo sapiens

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<400> 6
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Met Cys Cys Ala Val Ser Ile Trp Val Lys Ser Ile Arg Ile Cys Thr
20 25 30
Pro Met Gly Lys Leu Gly Asp Ser Cys His Pro Leu Thr Arg Lys Val
35 40 45
Pro Phe Phe Gly Arg Arg Met His His Thr Cys Pro Cys Leu Pro Gly
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50						55						60			
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Lys															

<210> 7
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 <212> PRT
 <213> Homo sapiens

<400> 7															
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Lys	Arg	Lys	Lys	Glu											
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<210> 8
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 <212> PRT
 <213> Homo sapiens

<400> 8															
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			20												

<210> 9
 <211> 19
 <212> PRT
 <213> Homo sapiens

<400> 9															
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Ser	Asp	Cys													

<210> 10
 <211> 26
 <212> PRT
 <213> Homo sapiens

<400> 10															
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Leu	Leu	Leu	Thr	Pro	Pro	Ala	Gly	Asp	Ala						
			20				25								

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<210> 11
 <211> 96
 <212> PRT
 <213> Bombina variegata

<400> 11
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 20 25 30
 Gly Ser Gly Thr Cys Cys Ala Ala Ser Ala Trp Ser Arg Asn Ile Arg
 35 40 45
 Phe Cys Ile Pro Leu Gly Asn Ser Gly Glu Asp Cys His Pro Ala Ser
 50 55 60
 His Lys Val Pro Tyr Asp Gly Lys Arg Leu Ser Ser Leu Cys Pro Cys
 65 70 75 80
 Lys Ser Gly Leu Thr Cys Ser Lys Ser Gly Glu Lys Phe Lys Cys Ser
 85 90 95

<210> 12
 <211> 81
 <212> PRT
 <213> Dendroaspis polylepis polylepis

<400> 12
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 1 5 10 15
 Thr Cys Cys Ala Val Ser Leu Trp Ile Lys Ser Val Arg Val Cys Thr
 20 25 30
 Pro Val Gly Thr Ser Gly Glu Asp Cys His Pro Ala Ser His Lys Ile
 35 40 45
 Pro Phe Ser Gly Gln Arg Lys Met His His Thr Cys Pro Cys Ala Pro
 50 55 60
 Asn Leu Ala Cys Val Gln Thr Ser Pro Lys Lys Phe Lys Cys Leu Ser
 65 70 75 80
 Lys

<210> 13
 <211> 81
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic construct

<400> 13
 Ala Val Ile Thr Gly Ala Cys Glu Arg Asp Val Gln Cys Gly Ala Gly
 1 5 10 15

10019101

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			20					25					30		
Pro	Leu	Gly	Arg	Glu	Gly	Glu	Glu	Cys	His	Pro	Gly	Ser	His	Lys	Val
		35				40					45				
Pro	Phe	Phe	Gly	Arg	Arg	Met	His	His	Thr	Cys	Pro	Cys	Leu	Pro	Gly
	50					55				60					
Leu	Ala	Cys	Leu	Arg	Thr	Ser	Phe	Asn	Arg	Phe	Ile	Cys	Leu	Ala	Gln
65					70					75					80
Lys															

<210> 14
 <211> 86
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic construct

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Met	Cys	Cys	Ala	Val	Ser	Ile	Trp	Val	Lys	Ser	Ile	Arg	Ile	Cys	Thr
			20					25				30			
Pro	Met	Gly	Lys	Leu	Gly	Asp	Ser	Cys	His	Pro	Leu	Thr	Arg	Lys	Val
		35				40					45				
Pro	Phe	Phe	Arg	Lys	Arg	Lys	His	His	Thr	Cys	Pro	Cys	Leu	Pro	Asn
	50					55				60					
Leu	Leu	Cys	Ser	Arg	Phe	Pro	Asp	Gly	Arg	Tyr	Arg	Cys	Ser	Met	Asp
65					70					75					80
Leu	Lys	Asn	Ile	Asn	Phe										
					85										

<210> 15
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic construct

Gly	Ile	Leu	Ala	Val	Ile	Thr	Gly	Ala	Cys	Glu	Arg	Asp	Val	Gln	Cys
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Gly	Ala	Gly	Thr	Cys	Cys	Ala	Ile	Ser	Leu	Trp	Leu	Arg	Gly	Leu	Arg
			20					25				30			
Met	Cys	Thr	Pro	Leu	Gly	Arg	Glu	Gly	Glu	Glu	Cys	His	Pro	Gly	Ser
		35				40					45				
His	Lys	Val	Pro	Phe	Phe	Arg	Lys	Arg	Lys	His	His	Thr	Cys	Pro	Cys
	50					55				60					
Leu	Pro	Asn	Leu	Leu	Cys	Ser	Arg	Phe	Pro	Asp	Gly	Arg	Tyr	Arg	Cys

80

<220>
<223> synthetic construct

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Leu Gly Arg Glu Gly Glu Glu Cys His Pro Gly Ser His Lys Val Pro
        35                          40                     45
Phe Phe Arg Lys Arg Lys His His Thr Cys Pro Cys Leu Pro Asn Leu
    50                          55                     60
Leu Cys Ser Arg Phe Pro Asp Gly Arg Tyr Arg Cys Ser Met Asp Leu
65                                70                    75                   80
Lys Asn Ile Asn Phe
                85
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<220>
<223> synthetic construct

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                20                25                30
Pro Leu Gly Arg Glu Gly Glu Glu Cys His Pro Gly Ser His Lys Val
                35                40                45
Pro Phe Phe Arg Lys Arg Lys His His Thr Cys Pro Cys Leu Pro Asn
                50                55                60
Leu Leu Cys Ser Arg Phe Pro Asp Gly Arg Tyr Arg Cys Ser Met Asp
65                70                75                80
Leu Lys Asn Ile Asn Phe
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<210> 18
<211> 87
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<212> PRT
<213> Artificial Sequence

<220>
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<400> 18
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20 25 30
Thr Pro Leu Gly Arg Glu Gly Glu Glu Cys His Pro Gly Ser His Lys
35 40 45
Val Pro Phe Phe Arg Lys Arg Lys His His Thr Cys Pro Cys Leu Pro
50 55 60
Asn Leu Leu Cys Ser Arg Phe Pro Asp Gly Arg Tyr Arg Cys Ser Met
65 70 75 80
Asp Leu Lys Asn Ile Asn Phe
85

<210> 19
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct

<400> 19
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1 5 10

10016481.1001